V. CLAIMS

What is claimed is:

1. A composition comprising nucleic acid comprising a transgene flanked by two terminal repeats and a nucleic acid enocoding an integrating enzyme under the control of a promoter element.

2. The composition of claim 1, wherein the promoter element is a promoter/enhancer.

3. The composition of claim 1, wherein the promoter is a site-specific promoter.

4. The composition of claim 3, wherein the site-specific promoter can be selected from at least the group consisting of the glial fibrillary acetic protein (GFAP) promoter, myolin basic (MBP) promoter, MCK promoter, NSE promoter, nestin promoter, synapsin promoter, Insulin 2 (Ins2) promoter, PSA promoter, albumin promoter, TRP-1 promoter, the tyrosinase promoter, the EIIA promoter, a promoter specific for breast tissue, such as the WAP promoter, a promoter specific for ovarian tissue, such as the ACTB promoter, or a promoter specific for bone tissue..

5. The composition of claim 1, wherein the promoter is inducible.

6. The composition of claim 5, wherein the inducible promoter can be selected from at least the group consisting of human heat shock promoter, Egr-1 promoter, tetracycline promoter, cre-lox recombinase system, and the human glandular kallilrien 2 (hK2) promoter.

7. The composition of claim 1, wherein the integrating enzyme can be selected from the group consisting of transposase, integrase, retrotransposase, recombinase, bacteriophage integrase, integron, terminase or retroviral integrase.

8. The composition of claim 7, wherein the integrating enzyme is a transposase.

9. The composition of claim 8, wherein the transposase can be selected from at least m the group consisting of Sleeping Beauty (SB), mos1, piggyback, Himar1, Hermes, Tol2 element, Pokey,

Tn7, Tn916, maT, Tc1/mariner and Tc3.

10. The composition of claim 7, wherein the integrating enzyme is a recombinase.

11. The composition of claim 10, wherein the recombinase is a site-specific recombinase.

12. The composition of claim 11, wherein the site-specific recombinase can be selected from the groups consisting of cre recombinase and tyrosine recombinase.

13. The composition of claim 7, wherein the integrating enzyme is a bacteriophage integrase.

14. The composition of claim 13, wherein the bacteriophage integrase can be selected at least from the group of bacteriopage consisting of lamda bacteriophage and mu bacteriophage.

15. The composition of claim 1, wherein the integrating enzyme is a chimeric integrating enzyme comprising a host-specific DNA binding domain.

16. The composition of claim 15, wherein the chimeric integrating enzyme is a chimeric transposase.

17. The composition of claim 15, wherein the chimeric integrating enzyme is a chimeric recombinase.

18. The composition of claim 1, wherein the host-specific binding domain of the chimeric integrating enzyme is fused to the transposases N-terminus.

19. The composition of claim 1, wherein the host-specific binding domain of the chimeric integrating enzyme is fused to the transposases C-terminus.

20. The composition of claim 1, wherein the integrating enzyme is located outside the terminal repeats.

21. The composition of claim 1, wherein the nucleic acid encoding the transgene and the nucleic

acid encoding the transposase are the same nucleic acid.

22. The composition of claim 1, wherein the nucleic acid encoding the transgene and the nucleic acid encoding the transposase are separate nucleic acids.

23. The composition of claim 1, further comprising a homologous sequence that is homologous to the host DNA.

24. The composition of claim 14, wherein the homologous sequence is located outside the terminal repeats.

25. The composition of claim 1, further comprising a protein binding sequence and a separate nucleic acid encoding two DNA binding domains.

26. The composition of claim 1, further comprising a protein binding sequence and a separate nucleic acid encoding a DNA binding domain and a protein-binding domain.